PC32099A_GPR35 SERQUENCE for NY(Identical to PC32099)
SEQUENCE LISTING

<110> Pfizer Inc.; Pfizer Japan Inc. (for Japan)

<120> GPR35

<130> PC32099

<160> 23

<170> PatentIn version 3.1

<210> 1
<211> 921
<212> DNA
<213> rat

<400> 1
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ttctgctatc gcatgcacca gtggacggag acccgagtct atatgaccaa cctggctgtg   180

gctgacgtct gcctgctctg ctccttgcca ttcgtgctgt actccctgaa atacagtact   240

tcggacacac ccatctgcca gctctcacag ggcatctacc tggtcaacag gtacatgagc   300

ataagcttgg tcaccgccat tgctgtggac cgctatgtgg cagtgcggca tcccctgcgt   360

gcccgtgagc tgcggtcccc acggcaggct ggagcagtgt gtgtggccct ctgggtgata   420

gtggtcacct ccctggtact cgcctggcgc ctgggggatac aggagggtgg cttctgcttc   480

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ccgctggcca tagtggtctt ctgctctttg caggttgtga ctgcgttggc ccgaaggcca   600

gccactgacg tggagcaggt ggaggccact cagaaggcca cccgcatggt ctgggccaac   660

ttggccgtgt ttatcatctg cttcctgccc ctgcatttga tcctgacagt gcaggtctcc   720

ctgaacctcc acacctgcgc tgcccgaaac atcttcagcc gtgccctgac aatcacagcc   780

aagctctcag acatcaactg ctgcctggat gccatctgtt actactacat ggccaaagag   840

ttccaggatg cgtccttgcg ggccacagcc tctagcacac cccacaagag ccaagatact   900

cagagcctga gcctcaccta g   921

<210> 2
<211> 306
<212> PRT
<213> rat

<400> 2

Met Asn Asn Thr Asn Cys Ser Ile Leu Pro Trp Pro Ala Ala Val Asn
1   5   10   15

His Ile Phe Thr Ile Tyr Leu Val Leu Leu Leu Val Leu Gly Leu Leu
            20   25   30

Leu Asn Gly Leu Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln Trp
        35   40   45

Thr Glu Thr Arg Val Tyr Met Thr Asn Leu Ala Val Ala Asp Val Cys
    50   55   60

Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser Thr

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| 65 | | | | 70 | | | | 75 | | | | 80 | | |

Ser Asp Thr Pro Ile Cys Gln Leu Ser Gln Gly Ile Tyr Leu Val Asn
           85   90   95

Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg Tyr
         100   105   110

Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro Arg
         115   120   125

Gln Ala Gly Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr Ser
  130   135   140

Leu Val Leu Arg Trp Arg Leu Gly Ile Gln Glu Gly Gly Phe Cys Phe
145   150   155   160

Ser Ser Gln Asn Arg Tyr Asn Phe Ser Thr Thr Ala Phe Ser Leu Leu
         165   170   175

Gly Phe Tyr Leu Pro Leu Ala Ile Val Val Phe Cys Ser Leu Gln Val
         180   185   190

Val Thr Ala Leu Ala Arg Arg Pro Ala Thr Asp Val Glu Gln Val Glu
         195   200   205

Ala Thr Gln Lys Ala Thr Arg Met Val Trp Ala Asn, Leu Ala Val Phe
  210   215   220

Ile Ile Cys Phe Leu Pro Leu His Leu Ile Leu Thr Val Gln Val Ser
225   230   235   240

Leu Asn Leu His Thr Cys Ala Ala Arg Asn Ile Phe Ser Arg Ala Leu
         245   250   255

Thr Ile Thr Ala Lys Leu Ser Asp Ile Asn Cys Cys Leu Asp Ala Ile
         260   265   270

Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Asp Ala Ser Leu Arg Ala
         275   280   285

Thr Ala Ser Ser Thr Pro His Lys Ser Gln Asp Thr Gln Ser Leu Ser
  290   295   300

Leu Thr
305

```
<210>   3
<211>   930
<212>   DNA
<213>   human

<400>   3
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gcgctctggg tgttctgctg ccgcatgcag cagtggacgg agacccgcat ctacatgacc     180
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aacctggcgg tggccgacct ctgcctgctg tgcaccttgc ccttcgtgct gcactccctg    240

cgagacacct cagacacgcc gctgtgccag ctctcccagg gcatctacct gaccaacagg    300

tacatgagca tcagcctggt catggccatc gccgtggacc gctatgtggc cgtgcggcac    360

ccgctgcgtg cccgcgggct gcggtccccc aggcaggctg cggccgtgtg cgcggtcctc    420

tgggtgctgg tcatcggctc cctggtggct cgctggctcc tggggattca ggagggcggc    480

ttctgcttca ggagcacccg gcacaatttc aactccatgg cgttcccgct gctgggattc    540

tacctgcccc tggccgtggt ggtcttctgc tccctgaagg tggtgactgc cctggcccag    600

aggccaccca ccgacgtggg gcaggcagag gccacccgca ggctgcccg catggtctgg    660

gccacctcc tggtgttcgt ggtctgcttc ctgccccctgc acgtggggct gacagtgcgc    720

ctcgcagtgg gctggaacgc ctgtgccctc ctggagacga tccgtcgcgc cctgtacata    780

accagcaagc tctcagatgc caactgctgc ctggacgcca tctgctacta ctacatggcc    840

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caggactctc tgtgcgtgac cctcgcctaa                                      930
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<210> 4
<211> 309
<212> PRT
<213> human

<400> 4

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Met Asn Gly Thr Tyr Asn Thr Cys Gly Ser Ser Asp Leu Thr Trp Pro
1               5                   10                  15


Pro Ala Ile Lys Leu Gly Phe Tyr Ala Tyr Leu Gly Val Leu Leu Val
            20                  25                  30


Leu Gly Leu Leu Leu Asn Ser Leu Ala Leu Trp Val Phe Cys Cys Arg
            35                  40                  45


Met Gln Gln Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val
        50                  55                  60


Ala Asp Leu Cys Leu Leu Cys Thr Leu Pro Phe Val Leu His Ser Leu
65                  70                  75                  80


Arg Asp Thr Ser Asp Thr Pro Leu Cys Gln Leu Ser Gln Gly Ile Tyr
                85                  90                  95


Leu Thr Asn Arg Tyr Met Ser Ile Ser Leu Val Met Ala Ile Ala Val
                100                 105                 110


Asp Arg Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Gly Leu Arg
            115                 120                 125


Ser Pro Arg Gln Ala Ala Ala Val Cys Ala Val Leu Trp Val Leu Val
            130                 135                 140


Ile Gly Ser Leu Val Ala Arg Trp Leu Leu Gly Ile Gln Glu Gly Gly
145                 150                 155                 160


Phe Cys Phe Arg Ser Thr Arg His Asn Phe Asn Ser Met Ala Phe Pro
```

PC32099A_GPR35 SERQUENCE for NY(Identical to PC32099)

```
            165                    170                 175
Leu Leu Gly Phe Tyr Leu Pro Leu Ala Val Val Val Phe Cys Ser Leu
            180                185                 190

Lys Val Val Thr Ala Leu Ala Gln Arg Pro Pro Thr Asp Val Gly Gln
        195                200                 205

Ala Glu Ala Thr Arg Lys Ala Ala Arg Met Val Trp Ala Asn Leu Leu
    210                215                220

Val Phe Val Val Cys Phe Leu Pro Leu His Val Gly Leu Thr Val Arg
225                230                235                240

Leu Ala Val Gly Trp Asn Ala Cys Ala Leu Leu Glu Thr Ile Arg Arg
                245                250                 255

Ala Leu Tyr Ile Thr Ser Lys Leu Ser Asp Ala Asn Cys Cys Leu Asp
            260                265                270

Ala Ile Cys Tyr Tyr Tyr Met Ala Lys Glu Phe Gln Glu Ala Ser Ala
            275                280                 285

Leu Ala Val Ala Pro Ser Ala Lys Ala His Lys Ser Gln Asp Ser Leu
    290                295                300

Cys Val Thr Leu Ala
305
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```
<210>   5
<211>   924
<212>   DNA
<213>   mouse

<400>   5
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atcatctact cagccttgct gctggtgctg ggcctgctgc tcaacagcgt ggcactctgg     120

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gtggccgacc tctgcctgct ctgctccttg ccatttgtgc tgtactccct gaaatatagt     240

tcttcagaca caccgtctg ccagctctca cagggcatct acctggccaa cagatacatg      300

agcataagcc tggtcactgc cattgctgtg accgctatg tggcagtgcg gcatcccctg       360

cgtgcgcgtg agctgcggtc cccgagacag gctgcagcag tgtgtgtggc cctttgggtg     420

atagtggtca cctccctggt agtgcgctgg cgcctgggga tgcaggaggg tggcttctgc     480

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ctgccgctgg ccatcgtggt cttctgctct ttgcaggtag tgactgtgct atcgagaagg     600

ccagccgctg atgtggggca ggcagaggcc acccaaaagg ccacccacat ggtctgggcc     660

aacttggctg tgtttgtcat ctgcttcctg cccttgcatg tggtcctgac cgtgcaggtc     720

tccctgaacc tcaatacctg tgctgcccga gacaccttca gccgtgccct gtccatcaca     780

ggtaaactct cagacaccaa ctgctgcctg gatgccatct gttactacta catggccaga     840

gagttccagg aagcgtccaa gccagccacg tcttccaaca cacccacaa gagccaagat      900
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tcccagatcc tgagcctcac ctag   924

<210> 6
<211> 307
<212> PRT
<213> mouse

<400> 6

Met Asn Ser Thr Thr Cys Asn Ser Thr Leu Thr Trp Pro Ala Ser Val
1   5   10   15.

Asn Asn Phe Phe Ile Ile Tyr Ser Ala Leu Leu Leu Val Leu Gly Leu
          20   25   30

Leu Leu Asn Ser Val Ala Leu Trp Val Phe Cys Tyr Arg Met His Gln
        35   40   45

Trp Thr Glu Thr Arg Ile Tyr Met Thr Asn Leu Ala Val Ala Asp Leu
      50   55   60

Cys Leu Leu Cys Ser Leu Pro Phe Val Leu Tyr Ser Leu Lys Tyr Ser
65   70   75   80

Ser Ser Asp Thr Pro Val Cys Gln Leu Ser Gln Gly Ile Tyr Leu Ala
              85   90   95

Asn Arg Tyr Met Ser Ile Ser Leu Val Thr Ala Ile Ala Val Asp Arg
          100   105   110

Tyr Val Ala Val Arg His Pro Leu Arg Ala Arg Glu Leu Arg Ser Pro
         115   120   125

Arg Gln Ala Ala Ala Val Cys Val Ala Leu Trp Val Ile Val Val Thr
     130   135   140

Ser Leu Val Val Arg Trp Arg Leu Gly Met Gln Glu Gly Gly Phe Cys
145   150   155   160

Phe Ser Ser Gln Thr Arg Arg Asn Phe Ser Thr Thr Ala Phe Ser Leu
              165   170   175

Leu Gly Phe Tyr Leu Pro Leu Ala Ile Val Val Phe Cys Ser Leu Gln
          180   185   190

Val Val Thr Val Leu Ser Arg Arg Pro Ala Ala Asp Val Gly Gln Ala
         195   200   205

Glu Ala Thr Gln Lys Ala Thr His Met Val Trp Ala Asn Leu Ala Val
     210   215   220

Phe Val Ile Cys Phe Leu Pro Leu His Val Val Leu Thr Val Gln Val
225   230   235   240

Ser Leu Asn Leu Asn Thr Cys Ala Ala Arg Asp Thr Phe Ser Arg Ala
              245   250   255

Leu Ser Ile Thr Gly Lys Leu Ser Asp Thr Asn Cys Cys Leu Asp Ala

PC32099A_GPR35 SERQUENCE for NY(Identical to PC32099)

```
           260                    265                 270
```

```
Ile Cys Tyr Tyr Tyr Met Ala Arg Glu Phe Gln Glu Ala Ser Lys Pro
           275             280                 285
```

```
Ala Thr Ser Ser Asn Thr Pro His Lys Ser Gln Asp Ser Gln Ile Leu
    290                 295                 300
```

```
Ser Leu Thr
305
```

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<210>  7
<211>  61
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

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t                                                                      61


<210>  8
<211>  30
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  8
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<210>  9
<211>  36
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  9
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<210>  10
<211>  40
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  10
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<210>  11
<211>  34
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  11
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PC32099A_GPR35 SERQUENCE for NY (Identical to PC32099)

```
<210>   12
<211>   23
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   12
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<210>   13
<211>   26
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   13
cacaggttcc tctggccctt ggcatg                                 26


<210>   14
<211>   36
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   14
ccccgaattc gccaccatga acaatacaaa ttgtag                      36


<210>   15
<211>   30
<212>   DNA
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<220>
<223>   primer

<400>   15
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<210>   16
<211>   25
<212>   DNA
<213>   Artificial Sequence

<220>
<223>   primer

<400>   16
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<210>   17
<211>   25
<212>   DNA
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<220>
<223>   primer

<400>   17
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<210>   18
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PC32099A_GPR35 SERQUENCE for NY(Identical to PC32099)

```
<211>  17
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  18
tgcaccacca actgctt                                               17


<210>  19
<211>  17
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  19
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<210>  20
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  20
aaattgtagc atcctcccgt ggcc                                       24


<210>  21
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  21
tatcttggct cttgtggggt gtgc                                       24


<210>  22
<211>  24
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  22
gtcttcacca ccatggagaa ggct                                       24


<210>  23
<211>  25
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  primer

<400>  23
gtgatggcat ggactgtggt catga                                      25
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